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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/730,465

DATE: 06/06/2001

TIME: 12:26:38

Input Set : A:\10274-006002.txt

Output Set: C:\CRF3\06062001\I730465.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

C--> 6 (i) APPLICANT: Wallner, Barbara P.
7 Cooper, Kevin D.
9 (ii) TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
10 Presenting Cell Driven Skin Conditions Using
11 Inhibitors of the CD2/LFA-3 Interaction
13 (iii) NUMBER OF SEQUENCES: 8
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: LAHIVE & COCKFIELD
17 (B) STREET: 60 State Street, Suite 510
18 (C) CITY: Boston
19 (D) STATE: Massachusetts
20 (E) COUNTRY: USA
21 (F) ZIP: 02109-1875
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/730,465
C--> 31 (B) FILING DATE: 05-Dec-2000
41 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: PCT/US92/08755
35 (B) FILING DATE: 06-OCT-1992
38 (A) APPLICATION NUMBER: US 07/862,022
39 (B) FILING DATE: 12-APR-1992
42 (A) APPLICATION NUMBER: US 07/770,969
43 (B) FILING DATE: 07-OCT-1991
45 (viii) ATTORNEY/AGENT INFORMATION:
46 (A) NAME: Myers, Louis (PLM)
47 (B) REGISTRATION NUMBER: 35,965
48 (C) REFERENCE/DOCKET NUMBER: BGP-111CP
50 (ix) TELECOMMUNICATION INFORMATION:
51 (A) TELEPHONE: (617)227-7400
52 (B) TELEFAX: (617)227-5941
55 (2) INFORMATION FOR SEQ ID NO: 1:
57 (i) SEQUENCE CHARACTERISTICS:
58 (A) LENGTH: 753 base pairs
59 (B) TYPE: nucleic acid
60 (C) STRANDEDNESS: single
61 (D) TOPOLOGY: linear
63 (ii) MOLECULE TYPE: cDNA
66 (ix) FEATURE:
67 (A) NAME/KEY: CDS
68 (B) LOCATION: 1..750

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70      (ix) FEATURE:
71          (A) NAME/KEY: sig_peptide
72          (B) LOCATION: 1..84
74      (ix) FEATURE:
75          (A) NAME/KEY: mat_peptide
76          (B) LOCATION: 85..750
78      (ix) FEATURE:
79          (A) NAME/KEY: misc_feature
80          (B) LOCATION: 1..750
81          (D) OTHER INFORMATION: /note= "Human transmembrane LFA-3"
83      (ix) FEATURE:
84          (A) NAME/KEY: misc_feature
85          (B) LOCATION: 646
86          (D) OTHER INFORMATION: /note= "Transmembrane domain"
89      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
91 ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG      48
92 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
93 -28          -25          -20          -15
95 GTC TGC CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT TTT TCC CAA CAA      96
96 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
97          -10          -5          1
99 ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA AGC AAT      144
100 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
101 5          10          15          20
103 GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA      192
104 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
105          25          30          35
107 GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG      240
108 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
109          40          45          50
111 GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA      288
112 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
113          55          60          65
115 TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT      336
116 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
117          70          75          80
119 ACC ATG AAG TTC TTT CTT TAT GTG CTT GAG TCT CTT CCA TCT CCC ACA      384
120 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
121 85          90          95          100
123 CTA ACT TGT GCA TTG ACT AAT GGA AGC ATT GAA GTC CAA TGC ATG ATA      432
124 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
125          105          110          115
127 CCA GAG CAT TAC AAC AGC CAT CGA GGA CTT ATA ATG TAC TCA TGG GAT      480
128 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
129          120          125          130
131 TGT CCT ATG GAG CAA TGT AAA CGT AAC TCA ACC AGT ATA TAT TTT AAG      528
132 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
133          135          140          145
135 ATG GAA AAT GAT CTT CCA CAA AAA ATA CAG TGT ACT CTT AGC AAT CCA      576

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136 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
137      150      155      160
139 TTA TTT AAT ACA ACA TCA ATC ATT TTG ACA ACC TGT ATC CCA AGC      624
140 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
141 165      170      175      180
143 AGC GGT CAT TCA AGA CAC AGA TAT GCA CTT ATA CCC ATA CCA TTA GCA      672
144 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
145      185      190      195
147 GTA ATT ACA ACA TGT ATT GTG CTG TAT ATG AAT GGT ATT CTG AAA TGT      720
148 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys
149      200      205      210
151 GAC AGA AAA CCA GAC AGA ACC AAC TCC AAT TGA      753
152 Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn
153      215      220
156 (2) INFORMATION FOR SEQ ID NO: 2:
158     (i) SEQUENCE CHARACTERISTICS:
159         (A) LENGTH: 250 amino acids
160         (B) TYPE: amino acid
161         (D) TOPOLOGY: linear
163     (ii) MOLECULE TYPE: protein
165     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
167 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
168 -28      -25      -20      -15
170 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
171      -10      -5      1
173 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
174 5      10      15      20
176 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
177      25      30      35
179 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
180      40      45      50
182 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
183      55      60      65
185 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
186      70      75      80
188 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
189 85      90      95      100
191 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
192      105      110      115
194 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
195      120      125      130
197 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
198      135      140      145
200 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
201      150      155      160
203 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
204 165      170      175      180
206 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
207      185      190      195

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```

209 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys
210           200           205           210
212 Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn
213           215           220
215 (2) INFORMATION FOR SEQ ID NO: 3:
217     (i) SEQUENCE CHARACTERISTICS:
218         (A) LENGTH: 723 base pairs
219         (B) TYPE: nucleic acid
220         (C) STRANDEDNESS: single
221         (D) TOPOLOGY: linear
223     (ii) MOLECULE TYPE: cDNA
226     (ix) FEATURE:
227         (A) NAME/KEY: CDS
228         (B) LOCATION: 1..720
230     (ix) FEATURE:
231         (A) NAME/KEY: sig_peptide
232         (B) LOCATION: 1..84
234     (ix) FEATURE:
235         (A) NAME/KEY: mat_peptide
236         (B) LOCATION: 85..720
238     (ix) FEATURE:
239         (A) NAME/KEY: misc_feature
240         (B) LOCATION: 1..720
241         (D) OTHER INFORMATION: /note= "Human PI-linked LFA-3"
243     (ix) FEATURE:
244         (A) NAME/KEY: misc_feature
245         (B) LOCATION: 568..720
246         (D) OTHER INFORMATION: /note= "Signal sequence for
247 PI-linkage"
250     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
252 ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG      48
253 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
254 -28      -25      -20      -15
256 GTC TGC CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT TTT TCC CAA CAA      96
257 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
258 -10      -5      1
260 ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA AGC AAT      144
261 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
262 5      10      15      20
264 GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA      192
265 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
266      25      30      35
268 GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG      240
269 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
270      40      45      50
272 GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA      288
273 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
274      55      60      65
276 TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT      336

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277 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
278      70      75      80
280 ACC ATG AAG TTC TTT CTT TAT GTG CTT GAG TCT CTT CCA TCT CCC ACA      384
281 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
282 85      90      95      100
284 CTA ACT TGT GCA TTG ACT AAT GGA AGC ATT GAA GTC CAA TGC ATG ATA      432
285 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
286      105      110      115
288 CCA GAG CAT TAC AAC AGC CAT CGA GGA CTT ATA ATG TAC TCA TGG GAT      480
289 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
290      120      125      130
292 TGT CCT ATG GAG CAA TGT AAA CGT AAC TCA ACC AGT ATA TAT TTT AAG      528
293 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
294      135      140      145
296 ATG GAA AAT GAT CTT CCA CAA AAA ATA CAG TGT ACT CTT AGC AAT CCA      576
297 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
298      150      155      160
300 TTA TTT AAT ACA ACA TCA TCA ATC ATT TTG ACA ACC TGT ATC CCA AGC      624
301 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
302 165      170      175      180
304 AGC GGT CAT TCA AGA CAC AGA TAT GCA CTT ATA CCC ATA CCA TTA GCA      672
305 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
306      185      190      195
308 GTA ATT ACA ACA TGT ATT GTG CTG TAT ATG AAT GGT ATG TAT GCT TTT      720
309 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Met Tyr Ala Phe
310      200      205      210
312 TAA      723
315 (2) INFORMATION FOR SEQ ID NO: 4:
317 (i) SEQUENCE CHARACTERISTICS:
318 (A) LENGTH: 240 amino acids
319 (B) TYPE: amino acid
320 (D) TOPOLOGY: linear
322 (ii) MOLECULE TYPE: protein
324 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
326 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
327 -28      -25      -20      -15
329 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
330      -10      -5      1
332 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
333 5      10      15      20
335 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
336      25      30      35
338 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
339      40      45      50
341 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
342      55      60      65
344 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
345      70      75      80
347 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/730,465

DATE: 06/06/2001

TIME: 12:26:39

Input Set : A:\10274-006002.txt

Output Set: C:\CRF3\06062001\I730465.raw

L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]